Claims

We Claim:

1. A method for determining a PCR amplified nucleic acid, said method comprising:
   a) contacting a sample comprising nucleic acid to be PCR amplified with at least one polymer comprising at least one linked energy donor moiety and at least one linked energy acceptor moiety wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence and wherein said polymer does not form a stem and loop hairpin and is further characterized in that the efficiency of transfer of energy between said donor and acceptor moieties, when the polymer is solvated in aqueous solution, is substantially independent of at least two variables selected from the group consisting of:
      i) nucleobase sequence length separating the at least one energy donor moiety from the at least one energy acceptor moiety;
      ii) spectral overlap of the at least one linked energy donor moiety and the at least one linked energy acceptor moiety;
      iii) presence or absence of magnesium in the aqueous solution; and the
      iv) ionic strength of the aqueous solution;
   b) contacting the sample with primers and other reagents for PCR amplification;
   c) PCR amplifying the nucleic acid;
   d) determining hybridization of the polymer to a target sequence within the amplified nucleic acid wherein the target sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the polymer; and
   e) determining the presence, absence or amount of PCR amplified nucleic acid in the sample.

2. The method of claim 1, wherein the nucleic acid to be amplified is contained within a plasmid.

3. The method of claim 1, wherein the PCR amplification is traditional.

4. The method of claim 1, wherein the PCR amplification is asymmetric.

5. The method of claim 1, wherein the PCR amplification is performed as a closed tube (homogeneous) assay.

6. The method of claim 1, wherein the amplified nucleic acid is quantitated.

7. The method of claim 1, wherein the presence or absence of the amplified nucleic acid is determined.

8. The method of claim 1, wherein the polymer is a peptide nucleic acid.

9. A method for determining a PCR amplified nucleic acid, said method comprising:

a) contacting a sample comprising nucleic acid to be PCR amplified with a polymer comprising:

i) a probing nucleobase sequence for probing a target sequence to which the probing nucleobase sequence is complementary or substantially complementary;

ii) at least one energy donor moiety that is linked to the probing nucleobase sequence; and

iii) at least one energy acceptor moiety that is linked to the probing nucleobase sequence wherein the at least one donor moiety is separated from the at least one acceptor moiety by at least a portion of the probing nucleobase sequence;

b) contacting the sample with primers and other reagents for PCR amplification;

c) PCR amplifying the nucleic acid;

d) determining hybridization of the polymer to a target sequence within the amplified nucleic acid wherein the target sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the polymer; and

e) determining the presence, absence or amount of PCR amplified nucleic acid in the sample.

10. The method of claim 9, wherein the nucleic acid to be amplified is contained within a plasmid.

11. The method of claim 9, wherein the PCR amplification is traditional.

12. The method of claim 9, wherein the PCR amplification is asymmetric.

13. The method of claim 9, wherein the PCR amplification is performed as a closed tube (homogeneous) assay.

14. The method of claim 9, wherein the amplified nucleic acid is quantitated.

15. The method of claim 9, wherein the presence or absence of the amplified nucleic acid is determined.

16. The method of claim 9, wherein the polymer is a peptide nucleic acid.